

Docket No.: TJU-2389

PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Waldman, S.A. *et al.*

Serial No.: 09/819,252

Group Art Unit: 1642

Filed: March 27, 2001

Examiner: Yu, Misook

Title: Compositions and methods for identifying and targeting cancer cells of alimentary canal origin

Assistant Commissioner for Patents
Washington, D.C. 20231

COPY

Dear Sir:

DECLARATION OF DR. SCOTT A. WALDMAN UNDER 37 CFR 1.132

I, Scott A. Waldman, M.D., Ph.D., do hereby declare:

1. I am the co-inventor of the subject matter claimed in the above-identified patent application.
2. Experiments were performed by me or by others in my laboratory under my supervision to compare the level of expression of Cdx2 in samples of normal esophagus and esophageal cancer samples.
3. Cdx2 mRNA and B-actin mRNA were quantified by quantitative RT-PCR (qRT-PCR) on 17 samples including 4 samples of esophageal cancer and 13 samples of normal esophagus. B-actin mRNA was quantified as a positive control.
4. The data is shown in Tables 1 and 2, attached hereto as Exhibits 1 and 2.

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5. The Y axis shows the ratio of Cdx2 expression to B-actin (Cdx2 copy #/B-actin copy #). The individual sample numbers are plotted on the X axis. In Table 1, the esophageal cancer samples assayed are shown as samples 1-4. The 13 normal esophagi assayed are shown as samples 7-19. Lanes 5-6 are blank.

6. The data in Table 2 demonstrate the expression of Cdx2 in the lowest-expressing esophageal tumor (Sample 2 in Table 1, which is Sample 1 in Table 2) compared to that in the 13 normal esophagi samples (Samples 2-14 in Table 2).

7. The data in Tables 1 and 2 demonstrate that Cdx2 is expressed in esophageal cancer but not in normal esophagus. The data in Table 1 show that the ratio of Cdx2 expression to B-actin expression is detectably higher for each cancer sample compared to each normal sample. Table 2 shows that even in the cancer sample with the lowest ratio, the ratio was significantly higher than that in the normal samples. The data in Tables 1 and 2 state that range of expression of Cdx2 (Cdx2 copy #/B-actin copy #) in tumors was 2.50-191.00 whereas in normal esophagus, it was 0.00-0.03. These data support the assertion that Cdx2 is expressed in esophageal cancer samples and not in normal esophagus samples.

8. A copy of the Abstract of Akashi Eda, Hiroyuki Osawa, Kiichi Satoh, Ichiro Yanaka, Ken Kihira, Yumiko Ishino, Hiroyuki Mutoh, Kentaro Sugano, Aberrant expression of CDX2 in Barrett's epithelium and inflammatory esophageal mucosa, Journal of Gastroenterology, Volume 38 Issue 1 (2003) pp 14-22 is attached hereto as Exhibit 3. The data reported therein indicate that Cdx2 is not expressed in normal esophagus.

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9. I hereby declare that all statements made herein are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment or both, under section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the applications and any patent issued thereon.

Date:

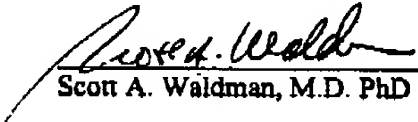

Scott A. Waldman, M.D. PhD

Exhibit 1: Table 1

Exhibit 2: Table 2

Exhibit 3: Abstract of Akashi Eda, Hiroyuki Osawa, Kiichi Satoh, Ichiro Yanaka, Ken Kihira, Yumiko Ishino, Hiroyuki Mutoh, Kentaro Sugano, Aberrant expression of CDX2 in Barrett's epithelium and inflammatory esophageal mucosa, Journal of Gastroenterology, Volume 38 Issue 1 (2003) pp 14-22

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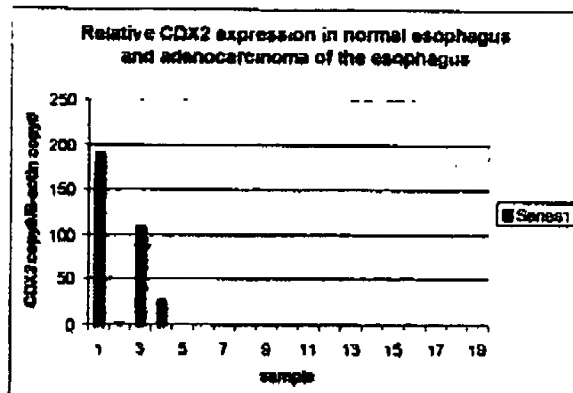
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EXHIBIT 1

Table 1



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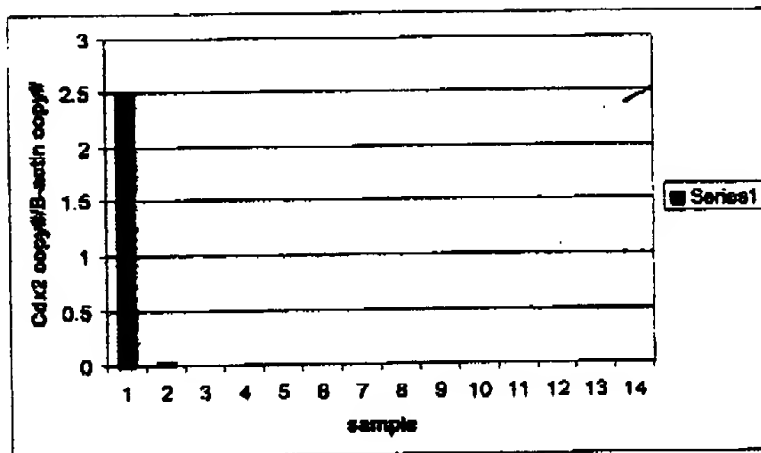
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EXHIBIT 2

Table 2



J. Gastroenterol 2002; 35:114

Gastroenterology
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Aberrant expression of *CDX2* in Barrett's epithelium and inflammatory esophageal mucosa

AKASHI EDA, HIROYUKI OSAWA, KIICHI SATOH, ICHIRO YANAKA, KEN KIHARA, YUMIKO ISHINO, HIROYUKI MUTOH, AND KENTARO SUGANO

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Background. There have been no detailed reports directly comparing the expression of *CDX1* with that of *CDX2* in the inflammatory esophageal mucosa and Barrett's epithelium. The present study was designed to examine the expression of *CDX1/2* in inflammatory esophageal mucosa with or without Barrett's epithelium. **Methods.** The expression of *CDX1/2* genes was analyzed using the reverse transcriptase-polymerase chain reaction (RT-PCR) in 34 human esophageal biopsy specimens, and *CDX2* expression was also evaluated immunohistochemically, using anti-human *CDX2* monoclonal antibody. The biopsy specimens for RNA extraction were taken endoscopically from esophageal mucosa with mucosal break due to gastroesophageal reflux disease (GERD), Barrett's epithelium, and normal epithelium. The expressions of mucin markers (*MUC2*) and intestine-specific genes (sucrase-isomaltase, human defensin-5, alkaline phosphatase) were also comparatively analyzed. **Results.** *CDX1/2* expression was not found in the normal esophageal mucosa. The prevalence of *CDX1/2* mRNA expression was significantly higher in the mucosa with Barrett's epithelium than in the mucosa without Barrett's epithelium. It is noteworthy, however, that the *CDX2* mRNA expression was initiated at the stage of esophagitis, when neither *CDX1* nor intestine-specific genes had emerged yet. In contrast to *CDX2*, *CDX1* was expressed only in Barrett's epithelium. Immunohistochemical study demonstrated strong and extensive nuclear immunoreactivity for *CDX2* in Barrett's epithelium. Furthermore, fine granular cytoplasmic staining was also observed in the cytoplasm in Barrett's epithelium, as well as in inflammatory esophageal mucosa. **Conclusions.** We report here, for the first time, that *CDX2* is expressed in patients with Barrett's epithelium and inflammatory

esophageal mucosa. These findings imply that the expression of *CDX2* may be an early event leading to the development of Barrett's esophagus.

Key words: Barrett's epithelium, *CDX1*, *CDX2*, gastroesophageal reflux disease

Introduction

The *CDX1* and *CDX2* genes are intestinal transcription factors that may be involved in the regulation of the proliferation and differentiation of intestinal epithelial cells. *CDX1/2* are members of the caudal-related homeobox gene family based on their sequence homology to the caudal gene of *Drosophila melanogaster*. The caudal gene is necessary for anteroposterior polarity during early *Drosophila* development.¹⁻⁴ *CDX1/2* protein is predominantly expressed in the intestine and colon, but not in the normal epithelium of the esophagus and stomach through adulthood in humans and mice.^{3,5-7}

Although Barrett's epithelium is classified into three types of columnar epithelia above the lower esophageal sphincter,⁸ the most specific distinguishing observation of Barrett's epithelium is the presence of specialized columnar epithelium with a villiform surface, mucous glands, and intestinal-type goblet cells, devoid of the brush-border characteristic of absorptive epithelium ("incomplete form" of intestinal metaplasia). In addition to this type, there is a complete type of intestinal metaplasia with brush-border and Paneth's cells, devoid of a villiform surface.

Many gene products, such as intestinal-type alkaline phosphatase (ALP);^{9,10} the well characterized brush-border enzyme, sucrase-isomaltase (SI),^{10,11} which is expressed in 76% of Barrett's esophagus;¹² human defensin-5 (HD),¹³⁻¹⁵ which is expressed predominantly

Received: March 12, 2002 / Accepted: May 31, 2002
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Aberrant *CDX2* expression in the esophagus

in Paneth's cells; and mucus-secreting goblet cell-mucin marker (*MUC2*)^{19,20} are associated with gastric and esophageal intestinal metaplasia.

Barrett's mucosa is often associated with chronic gastroesophageal reflux disease (GERD),^{18,20} but genetic events predisposing to Barrett's mucosa are not well documented. We have reported that the expression of *CDX2* precedes those of *CDX1*, *S1*, other intestine-specific genes (*HD*, *ALP*) and *MUC2* during the progression of gastric intestinal metaplasia.²¹ Furthermore, we confirmed the aberrant *CDX2* expression in chronic gastritis and intestinal metaplasia using immunohistochemistry.²² Our findings imply that the expression of *CDX2* is initiated at the stage of chronic gastritis, and the expression of *CDX2* may not be the result of, but the trigger for, the chronic gastritis/metaplasia transition in the stomach. Furthermore, we generated a transgenic mouse in which intestinal metaplasia was induced by expressing *CDX2* in the stomach.²³ Therefore, we consider that *CDX2* expression may play a critical role in the development of intestinal metaplasia.

A previous investigation showed that *CDX1* was also expressed in the intestinal metaplasia of the esophagus, stomach,^{24,25} and bile duct.²⁶ However, *CDX2* expression has not been studied comparatively with that of *CDX1*, nor with that of intestine-specific marker genes.

Accordingly, we focused on specialized columnar epithelium and examined the expression patterns of *CDX1/2* in inflammatory esophageal epithelium and Barrett's epithelium, in order to gain insight into the role of these homeotic genes in the progression of Barrett's epithelium.

Subjects and methods

Ethical approval

The study was approved by the Ethics Committee of the Jichi Medical School, Japan. Written informed consent was obtained from all patients.

Human esophageal tissue samples

We studied 34 patients who underwent routine upper endoscopy with biopsies at the Department of Gastroenterology, Jichi Medical School. Biopsy samples were immediately snap-frozen in liquid nitrogen and then stored at -80°C until processed.

Endoscopy with biopsy

Barrett's epithelium was defined endoscopically as any tongues of pink mucosa and/or circumferential columnar-appearing mucosa proximal to the esophago-

cardiac junction (ECJ). The ECJ was determined endoscopically, using the definition of the ECJ as the distal end of the fine longitudinal vessels recommended by Hoshuhara et al.²⁶

Short-segment Barrett's esophagus (SSBE) and long-segment Barrett's esophagus (LSBE) were defined as a length of less than 3 cm and a length of 3 cm or more 3 cm, respectively, of columnar epithelium above the SCJ at endoscopy.^{27,28} Endoscopic assessment of GERD was performed using the Los Angeles (LA) classification.²⁹

Diagnosis of Barrett's epithelium

Features of Barrett's epithelium were judged based on molecular findings. Barrett's epithelium (specialized columnar epithelium) was judged to be present when there was expression of more than one of the gene markers for intestinal metaplasia (*HD*, *ALP*, and *MUC2*), in addition to *S1* mRNA being detected.

In all patients, one biopsy specimen for RNA extraction was taken endoscopically from the esophageal mucosa proximal to the ECJ, with or without mucosal break, or from Barrett's epithelium.

In addition, in 15 patients, for comparative study with immunohistochemistry, one set of two side-by-side biopsy specimens was taken endoscopically from normal esophageal epithelium, inflammatory esophageal mucosa with mucosal break due to gastroesophageal reflux disease (GERD), and from Barrett's epithelium. RNA extraction was performed on one of the two biopsy samples, while the other sample was analyzed histologically (hematoxylin-and-eosin stain) and immunohistochemically. Biopsy specimens for histological analysis were fixed in 10% buffered formalin, embedded in paraffin, and stained with hematoxylin and eosin. Esophageal specimens were evaluated for the presence or absence of histological intestinal metaplasia and esophagitis.

Immunohistochemistry

The sections used for *CDX2* immunohistochemistry were paraffin-embedded sections that were deparaffinized in xylene and treated with 3% hydrogen peroxide in methanol for 5 min to block endogenous peroxidase. The sections were immersed in citrate buffer (10 mM, pH 6.0) and heated for 20 min at 120°C in an autoclave. After the heating, the specimens were cooled for 60 min at room temperature. After incubation with blocking reagent (Dako Japan, Kyoto, Japan) for 10 min to eliminate non-specific staining, the sections were incubated with *CDX2* monoclonal antibody to anti-human *CDX2* protein (diluted 1:100; BioGenex, San Ramon, CA, USA) in a moist chamber overnight at

4°C. This CDX2 antibody reacts with a conserved epitope of the 40-kDa human CDX2 protein, according to the manufacturer. Then the sections were incubated with Dextran polymer system/ peroxidase (EnVision™; Dako Japan) for 90 min at room temperature. The color of immunostaining was developed with diaminobenzidine solution for 6–8 min, and the sections were counterstained with hematoxylin. The biopsy specimens of gastric intestinal metaplasia served as positive controls. For the negative control, sections were incubated with normal mouse IgG1, and no immunoreactivity was observed.

RNA extraction and reverse transcriptase-polymerase chain reaction (RT-PCR)

Specific primers were designed for the *CDX1/2*, mucin marker (*MUC2*), and the intestinal metaplasia-associated antigenic molecules (*SI*, *HD*, and *ALP*). The primers used are listed in Table 1. The primer pairs for *CDX1/2* were designed to be located in different exons of the respective genes to exclude the effect of contamination by genomic DNA. Total RNA was isolated from tissues with Isogen (Nippon Gene, Tokyo, Japan), according to the protocols recommended by the manufacturer. Two micrograms of total RNA was reverse transcribed with random nanomers and reverse transcriptase (ReverTraAce; Toyobo, Osaka, Japan) following the conditions of the manufacturer.

The template cDNAs were amplified with Taq polymerase in the presence of the primer set. The thermocycling parameters used in the PCR were as follows: denaturation, 30 s at 94°C; annealing, 30 s at 54°C (63°C for *CDX1*, 60°C for *CDX2*); and extension, 30 s at 72°C. These reactions were repeated for 35 cycles. The PCR products were electrophoresed through a 2.0% agarose gel and stained with ethidium bromide. Similarly, glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) was amplified as an internal control. We confirmed the nucleotide sequences of the RT-PCR products by direct sequencing (data not shown).

Statistical analysis

Fisher's exact test was used to assess differences in the frequency of *CDX1/2* expression among the various groups shown in the contingency tables. A computed two-tailed *P* value of less than 0.05 was regarded as indicating statistical significance.

Results

Clinical and histological characteristics

Clinicopathological findings of the subjects are summarized in Table 2. The mean age of the patients was 54.7 years (range, 34–77 years), and the ratio of men to women was 16:18.

The patients were classified into three groups. Five patients who showed normal ECJ endoscopically and histologically were assigned to group N (specimens 30–34; mean age 55.2 years; men/women, 3:2). Fourteen patients assessed as having intestinal metaplasia, based on molecular findings, were assigned to the Barrett's epithelium group (specimens 1–14; mean age, 57 years; men/women, 5:9). All Barrett's epithelium was defined as SSBE at endoscopy. Fifteen patients assessed as lacking intestinal metaplasia, based on molecular findings, who showed esophagitis endoscopically were assigned to the GERD group (specimens 15–29; mean age, 52.4 years; men/women, 8:7). Endoscopic findings of GERD ranged from A to C, using the LA classification.

RT-PCR analysis

All the results of RT-PCR are listed in Table 2 and shown in Fig. 1. None of the intestinal gene markers was expressed in group N subjects. Neither *CDX1* nor *CDX2* was detectable (0/5) in the esophageal mucosa of group N patients.

The prevalence of *CDX1* mRNA expression in the esophageal mucosa was significantly higher in the mucosa with intestinal metaplasia than in the mucosa

Table 1. Primer pairs used in polymerase chain reactions (PCRs)

Genes	Primer pairs	
	Sense (5' to 3')	Antisense (5' to 3')
<i>CDX1</i>	AGCCGTTACATCACAATC	GAGACTCGGACCAGACCT
<i>CDX2</i>	GAGCTGGAGAAGGAGTTT	GGTGACGGTGGGGTTTAG
<i>Sucrase</i>	TGGCAAGAAAGAAATTTAGTGA	TTATTCTCACATTGACAGGATC
<i>Defensin-5</i>	ATGAGGACCATCGCCATCCT	TCAGCGACAGCAGAGTCTGTAG
<i>ALP</i>	TGCAGGGGGCCCTGGGTG	GCGTAGGTGCCGGCTGG
<i>MUC2</i>	ACAACACTCCTCTACCTCCA	GTTGATCTCGTAGTTGAGGCA
<i>GAPDH</i>	CCACCCATGGCAAATTCATGGCA	TCTAGACGGCAGGTCAGGTCCACC

Sucrase, sucrase-isomaltase; *defensin-5*, human defensin-5; *ALP*, alkaline phosphatase; *MUC2*, mucin marker; *GAPDH*, glyceraldehyde-3-phosphate dehydrogenase.

A. Expression of *CDX2* expression in the esophagus

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Table 2. Summary of gene expression in 34 samples

Case no	Age (years)/sex	Endoscopic findings	Reverse transcriptase (RT)-PCR					
			CDX1	CDX2	MUC2	Sucrase	Defensin	ALP
Barrett's epithelium (n = 14)								
1	45/M	SSBE	-	+	+	-	+	+
2	53/F	SSBE	+	+	+	-	-	-
3	44/F	SSBE	-	+	+	-	-	-
4	53/F	SSBE	+	+	+	+	+	+
5	70/M	SSBE	-	+	+	+	-	-
6	43/F	SSBE	-	+	+	+	-	-
7	64/F	SSBE	+	+	+	+	+	+
8	48/F	SSBE	-	+	+	+	-	-
9	56/F	SSBE	-	+	+	+	+	+
10	71/M	SSBE	+	+	-	+	+	+
11	47/F	SSBE	+	+	+	+	-	-
12	61/M	SSBE	+	+	+	+	-	-
13	66/M	SSBE	-	+	-	+	+	-
14	77/F	SSBE	+	+	-	+	-	-
GERD (n = 15)								
15	39/F	LA: A	-	+	-	-	-	-
16	76/M	LA: B	-	+	-	+	-	-
17	62/M	LA: A	-	-	-	-	-	-
18	67/F	LA: C	-	+	-	-	-	-
19	58/M	LA: B	-	+	-	-	-	-
20	64/M	LA: A	-	+	-	-	-	-
21	75/F	LA: C	-	-	-	-	-	-
22	44/F	LA: C	-	+	+	-	-	-
23	34/F	LA: B	-	-	-	-	-	-
24	50/M	LA: A	-	-	+	-	-	+
25	58/M	LA: A	-	+	-	-	-	-
26	37/F	LA: A	-	+	-	+	-	-
27	42/F	LA: A	-	+	-	-	-	-
28	38/M	LA: B	-	+	-	+	-	-
29	43/M	LA: A	-	-	-	+	-	-
Group N (n = 5)								
30	43/M	Normal	-	-	-	-	-	-
31	36/M	Normal	-	-	-	-	-	-
32	65/F	Normal	-	-	-	-	-	-
33	56/F	Normal	-	-	-	-	-	-
34	76/M	Normal	-	-	-	-	-	-

Sucrase, sucrase-isomaltase; ALP, alkaline phosphatase; SSBE, short-segment Barrett's esophagus; LA, Los Angeles classification; GERD, gastroesophageal reflux disease

without intestinal metaplasia (57% [8/14] vs 0% [0/15]; $P < 0.001$) (Fig. 2).

The prevalence of *CDX2* mRNA expression in the esophageal mucosa was also significantly higher in the mucosa with intestinal metaplasia than in the mucosa without intestinal metaplasia (100% [14/14] vs 67% [10/15], $P < 0.001$) (Fig. 2).

Coexpression of *CDX1* and *CDX2* was observed in 57% (8/14) of the Barrett's epithelium. It is of note that the expression of *CDX2* emerged at the stage of esophagitis without expression of *CDX1* or gene markers for intestinal metaplasia (Fig. 2). In contrast to *CDX2*, *CDX1* was expressed only in Barrett's epithelium.

Immunohistochemistry

No immunoreactivity for *CDX2* was observed in normal esophageal epithelium (Fig. 3).

Immunohistochemical study demonstrated strong nuclear immunoreactivity for *CDX2* in an extensive area of Barrett's epithelium (Fig. 4). Furthermore, fine granular cytoplasmic staining was also observed in Barrett's epithelium, as well as in inflammatory esophageal mucosa, including both squamous mucosa and submucosal glands (Figs. 4, 5, 6). These staining patterns were not detected in the negative controls, or in the normal esophageal mucosa (Fig. 3, Table 2). The concordance rate between the histological presence

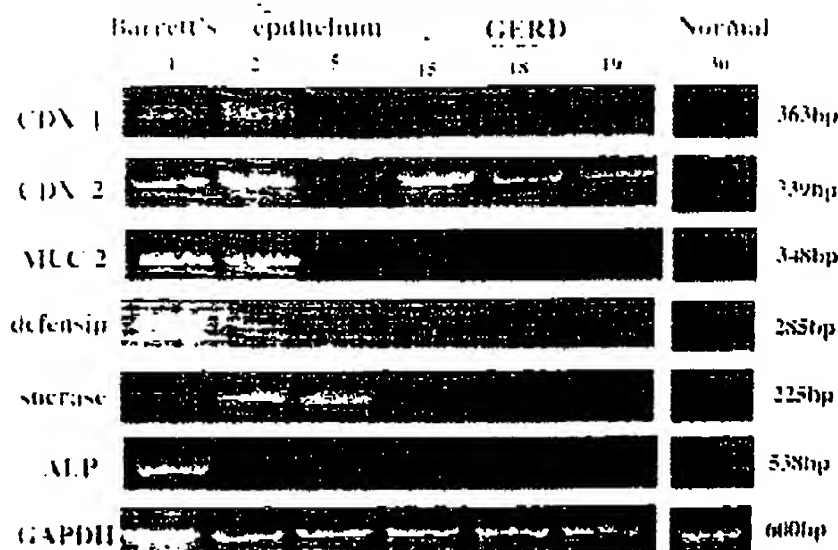


Fig. 1. Reverse transcriptase-polymerase chain reaction (RT-PCR) analysis of *CDX1/2*, mucin marker (*MUC2*), and intestinal metaplasia-associated antigenic molecules (human defensin-5 [*HD*], sucrase-isomaltase [*SI*], alkaline phosphatase [*ALP*]). Left, Genes; right, sizes of the PCR products. Lane numbers corresponds to Table 2 numbers. The results are summarized in Table 2. GERD, Gastroesophageal reflux disease; GAPDH, glyceraldehyde 3-phosphate dehydrogenase.

Expression of CDX1/2 in esophagus

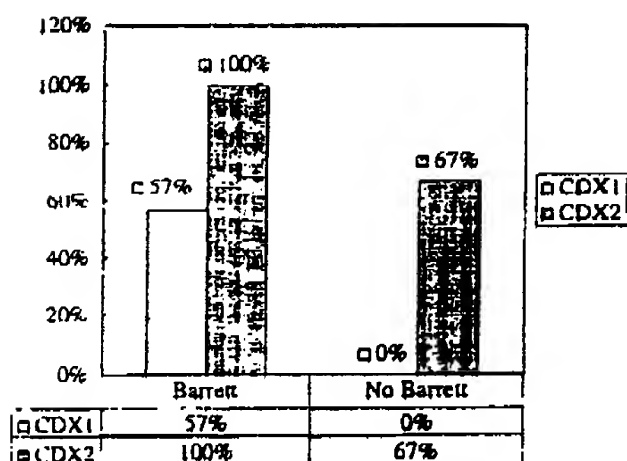


Fig. 2. Prevalence of *CDX1/2* expression in the esophageal mucosa. Expression of *CDX2* emerged in the esophageal mucosa without expression of *CDX1* and gene markers for intestinal metaplasia. The prevalence of *CDX1/2* mRNA expression was significantly higher in the mucosa with Barrett's epithelium than in the mucosa without Barrett's epithelium.

of intestinal metaplasia (hematoxylin-and-eosin stain) and that diagnosed based on molecular findings was 87% (Table 3). The concordance rate between the presence of *CDX2* expression determined by RT-PCR and immunohistochemical positivity was 100% (Table 3).

Discussion

The intestine-specific transcription factors *CDX1* and *CDX2* are important in the early differentiation and maintenance of intestinal epithelial cells during gastrointestinal development.^{20,21}

In intestinal metaplasia, gastric and esophageal epithelial cells undergo changes that transform the cells into different phenotypes. The sequence of genetic events during the progression from normal epithelium to intestinal metaplasia is still unclear.

Many gene products, such as *ALP*, *SI*, *HD*, and *MUC2*, are expressed in intestinal metaplasia. It has been proposed that *CDX1* may play an important role in this transdifferentiation.²² Epithelial cells in intestinal metaplasia of the gastric mucosa express the *CDX1* protein, whereas normal gastric mucosa adjacent to areas of intestinal metaplasia has been immunohistochemically shown not to express *CDX1*.^{24,25}

However, in addition to *CDX1*, the homologous transcriptional factor, *CDX2*, may also participate in this process.

Nevertheless, there has been no report about the detailed time sequence, i.e., when and how these gene expressions are evoked during the process of intestinal metaplasia. This study analyzed the complex patterns of expression of *CDX1* and *CDX2* during the development of Barrett's epithelium.

The *CDX1/2* expression rates appeared to be associated with the transition from GERD to Barrett's esophagus. In contrast to *CDX1*, *CDX2* was already expressed in inflammatory esophageal mucosa with-

Figure 3. CDX2 expression in the esophagus



Fig. 3. Immunohistochemical study for CDX2 protein in normal esophageal epithelium. No immunoreactivity for CDX2 was observed in normal epithelium. $\times 200$



Fig. 4. Immunohistochemical demonstration of CDX2 protein in Barrett's epithelium. Strong nuclear immunoreactivity for CDX2 was observed in metaplastic glands. $\times 500$

out the expression of gene markers for intestinal metaplasia.

The sequential pattern of gene expression demonstrated in the present study accorded with the scenario of the interaction among the intestine-specific genes *in vitro*. Our data show that the expression of *CDX2* occurred in the absence of *CDX1*, other intestine-specific genes (*S1*, *HD*, *ALP*), and *MUC2*. This pattern is consistent with the result that *CDX2* expression in Caco-2 cells induces the expression of *S1* and lactase-phlorizin hydrolase, markers of intestinal differentiation *in vitro*.¹² Both *S1* and lactase-phlorizin hydrolase promot-

ers are activated by Cdx proteins.¹²⁻²⁴ Functional studies have also shown *CDX2* to regulate intestine-specific gene transcription *in vivo*, as evidenced by binding to several intestine-specific promoters and the activation of transcription.²⁴⁻²⁷ Our finding implies that the expression of *CDX2* may not be the result of, but the trigger for, the development of intestinal metaplasia.

A set of two separate biopsy specimens for RNA extraction and histological examination may not be optimal for the detection and analysis of intestinal metaplasia,²⁸ because intestinal metaplasia is multifocal, and the possibility cannot be denied that sampling error may

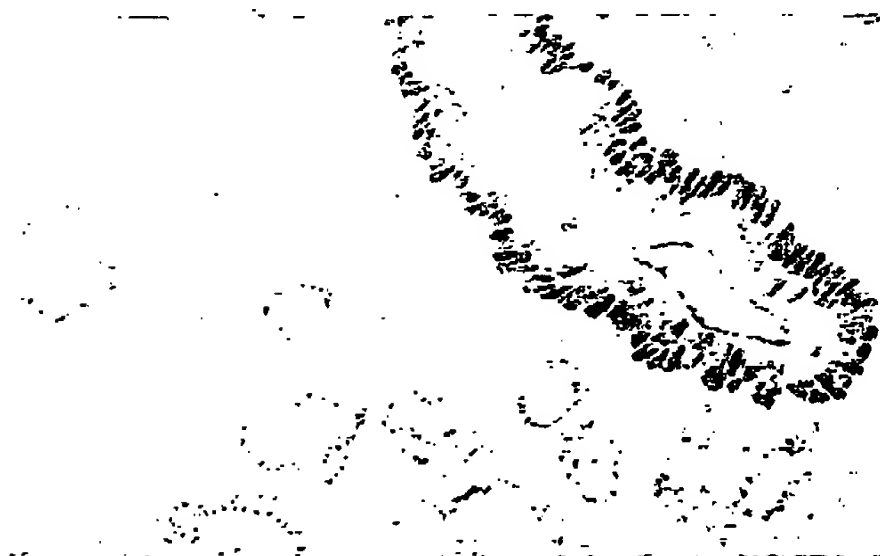


Fig. 5. Immunohistochemical demonstration of CDX2 protein in Barrett's epithelium. Strong nuclear immunoreactivity for CDX2 was observed in metaplastic glands, and cytoplasmic immunoreactivity for CDX2 was seen in submucosal glands. $\times 500$



Fig. 6. Inflammatory esophageal squamous mucosa, characterized by fine granular cytoplasmic immunoreactivity for CDX2. $\times 200$

tissue even if two adjacent biopsy samples are taken side by side.

Consequently, we characterized the specimens based on molecular findings and correlated *CDX1/2* expression with gene markers for intestinal metaplasia. As a result, the concordance rate between the histological presence of intestinal metaplasia and that diagnosed based on molecular findings was 87%. The concordance rate between the presence of *CDX2* expression, determined by RT-PCR, and immunohistochemical positivity was 100%. These results suggest that the *CDX2* expression rate in esophagus is high at the stage of esophagitis.

The sequential pattern of the relative expression of *CDX1/2* in metaplastic lesions may hold true across the differences in organs, between the esophagus and stomach. Namely, the sequential pattern of the expression of *CDX1/2* in the development of Barrett's epithelium is the same as that seen in the development of gastric intestinal metaplasia. In chronic gastritis, *CDX2* was expressed in the antral and fundic mucosa in the absence of expression of *CDX1* and gene markers for intestinal metaplasia (*SI*, *HD*, *ALP*, and *MUC2*) and hence, the expression of *CDX2* precedes those of *CDX1* and these intestine-specific genes during the progression of intestinal metaplasia.² Furthermore,

Eda et al. *CDX2* expression in the esophagus

Table 3. Summary of histology, RT-PCR, and immunohistochemistry (IHC) for *CDX2* in 15 samples

in 15 samples		CDX2 expression		
Case number*	Histology Intestinal metaplasia	RT-PCR	IHC	
Barrett's epithelium (n = 5)				
1	+	+	+	(Nuclear)
2	+	+	+	(Nuclear)
3	-	+	+	(Cytoplasmic)
4	+	+	+	(Nuclear)
5	-	+	+	(Cytoplasmic)
GERD (n = 5)				
15	-	+	+	(Cytoplasmic)
16	-	+	+	(Cytoplasmic)
17	-	-	-	-
18	-	+	+	(Cytoplasmic)
19	-	+	+	(Cytoplasmic)
Group N (n = 5)				
30	-	-	-	-
31	-	-	-	-
32	-	-	-	-
33	-	-	-	-
34	-	-	-	-

*Case number corresponds to Table 2 number

we have confirmed the aberrant *CDX2* expression in chronic gastritis and intestinal metaplasia using immunohistochemistry.²²

Barrett's epithelium is presumed to be the result of chronic inflammation caused by the gastric and duodenal juice, including bile, that flows back into the esophagus, whereas, it is presumed that gastric metaplasia is the terminal state of chronic gastritis caused by *H. pylori*. Therefore, any inflammation, irrespective of the cause, may play an important role in the induction of *CDX2* expression in the initiation of intestinal metaplasia in the esophageal and gastric mucosa.

In the GERD group, the expression of MUC2 and sucrase was positive in a few cases (cases 16, 22, 24, 26, and 28 in Table 2) by RT-PCR. These findings may result from the contamination of metaplastic cells. So, we analyzed *CDX2* expression immunohistochemically to determine the precise localization of the *CDX2* protein in the inflammatory esophageal mucosa and Barrett's esophagus. As a result, the immunohistochemical study demonstrated strong nuclear immunoreactivity for *CDX2* in Barrett's epithelium. In contrast, perinuclear immunoreactivity for *CDX2* was detected in the inflammatory esophageal mucosa, including both squamous mucosa and submucosal glands. During the progression from GERD to Barrett's esophagus, the localization of *CDX2* protein may shift from cytoplasm to nucleus. The genetic mechanisms and candidate factors involved in this process should be explored in future. These data will provide insight into

abnormal gene expression in the esophagitis/Barrett's esophagus transition.

It cannot be concluded that *CDX1/2* expression is the sole cause of intestinal metaplasia, based on the data shown here. However, we generated a transgenic mouse in which intestinal metaplasia was induced by expressing *CDX2* in the stomach.²³ Therefore, we consider that *CDX2* expression may play a critical role in the development of intestinal metaplasia.

In conclusion, we demonstrated here that the *CDX2* homeodomain protein was ectopically overexpressed in Barrett's epithelium and inflammatory esophageal mucosa. These findings suggest that the expression of *CDX2* may be the crucial event leading to the progression of Barrett's esophagus, and that *CDX2* expression precedes that of *CDX1*, *SI*, other intestine-specific genes (*HD*, *ALP*), and *MUC2*.

Acknowledgments. We thank Ms K. Sasaki for her excellent technical assistance. This study was supported in part by a Grant-in-Aid for Scientific Research(B) No. 13470122 from the Japanese Ministry of Education, Culture, Sports, and Technology.

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**Applicant(s) :
Title:**

Waldman, S.A. et al.
Compositions And Methods For Identifying And Targeting
Cancer Cells Of Alimentary Canal Origin

Application No.:

09/819,252

Filed:

March 27, 2001

Docket No.:

TJU-2389

Date Sent:

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